

11/16 0840/0420

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/915,543

DATE: 11/16/2001

TIME: 08:29:01

Input Set : A:\es.txt

Output Set: N:\CRF3\11162001\I915543.raw

ENTERED

3 <110> APPLICANT: BASLER, Konrad
 4 BRUNNER, Erich
 5 FROESCH, Barbara
 6 KRAMPS, Thomas
 7 PETER, Oliver
 9 <120> TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING
 PATHWAY AND
 10 THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON
 12 <130> FILE REFERENCE: Q60361
 14 <140> CURRENT APPLICATION NUMBER: 09/915,543
 15 <141> CURRENT FILING DATE: 2001-07-27
 17 <150> PRIOR APPLICATION NUMBER: 60/221,502
 18 <151> PRIOR FILING DATE: 2000-07-28
 20 <160> NUMBER OF SEQ ID NOS: 22
 22 <170> SOFTWARE: PatentIn version 3.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 6909
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Drosophila lgs
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 31 <222> LOCATION: (691)..(981)
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 62 <223> OTHER INFORMATION:
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 68 cctgctaaca taacgcacgg ttaaaggcagg aacatttggg cctataagcc caaaatttca 120
 70 ttagcttaat acgatgtcc gaagtgttat tgcatttgca catatacata aaatttgac 180
 72 atagaatagg agaattccac atacaataac aaaaatacaa aatcctccag taaaatttaa 240

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74 aacgatatcg	tgtttgtt	cgcgtatctc	acgtgagatg	taatcgcatg	catatgagtg	300
76 gtgagtgcc	tgcgtgcagg	tctggctaa	atatgcctaa	ttgcgttcgc	cgacttcaa	360
78 agcaataaaa	cgatggattt	taattgtcac	ttgagcaatt	agccacacaa	gggatcttgg	420
80 gaaggtcgat	ttgaaggaat	tcgatttcta	ggatgtctc	gacaaca	atg ccc cgc	476
81					Met Pro Arg	
82					1	
84 agt cca acc	caa caa cag	ccg caa cca	aac tcc gat	gcc tcc tca	aca	524
85 Ser Pro Thr	Gln Gln Gln	Pro Gln Pro	Asn Ser Asp	Ala Ser Ser	Thr	
86 5	10	15				
88 agt gca tct	gga tca aat	cct gga gca	gct atc gga	aat ggg gac	tcg	572
89 Ser Ala Ser	Gly Ser Asn	Pro Gly Ala	Ala Ile	Gly Asn Gly	Asp Ser	
90 20	25	30	35			
92 gcg gcg agc	aga agt tct	ccg aag acc	ctt aat agc	gaa ccc ttt	tct	620
93 Ala Ala Ser	Arg Ser Ser	Pro Lys Thr	Leu Asn Ser	Glu Pro Phe	Ser	
94 40	45	50				
96 act ttg tcg	ccg ggtaagactt	gtattgattt	ctctttgtcc	ggaattataa		672
97 Thr Leu Ser	Pro					
98 55						
100 caactttctg	tgtttcca	gat caa ata	aaa ttg acg	cca gaa gaa	ggc act	723
101		Asp Gln Ile	Lys Leu Thr	Pro Glu Glu	Gly Thr	
102		60	65			
104 gag aaa agc	gga cta tca	act agt gat	aaa gct gcc	act gga gga	gcc	771
105 Glu Lys Ser	Gly Leu Ser	Thr Ser Asp	Lys Ala Ala	Thr Gly Gly	Ala	
106 70	75	80				
108 cca ggc agt	gga aat aat	ctg ccc gag	gga caa act	atg cta agg	cag	819
109 Pro Gly Ser	Gly Asn Asn	Leu Pro Glu	Gly Gln Thr	Met Leu Arg	Gln	
110 85	90	95				
112 aac tct acg	agc aca atc	aac tcg tgc	cta gtc gct	tct cca caa	aac	867
113 Asn Ser Thr	Ser Thr Ile	Asn Ser Cys	Leu Val Ala	Ser Pro Gln	Asn	
114 100	105	110				
116 tcc agt gaa	cac tcg aat	agc agc aat	gtg tct	gct aca gtg	ggc ctt	915
117 Ser Ser Glu	His Ser Asn	Ser Ser Asn	Val Ser Ala	Thr Val Gly	Leu	
118 115	120	125	130			
120 act cag atg	gta gat tgt	gac gag caa	tcg aag aaa	aac aaa tgt	agt	963
121 Thr Gln Met	Val Asp Cys	Asp Gln Ser	Lys Lys Asn	Lys Cys	Ser	
122 135	140	145				
124 gtg aag gac	gag gaa gct	ggtaagactg	ccctacaaat	ggttaaaaat		1011
125 Val Lys Asp	Glu Glu Ala					
126 150						
128 tttaaatgt	attggcggttc	acctttgtta	atcatttaat	tgtttttttt	ttgctatact	1071
130 tacaatttta	gttttaaact	tgtaaacttgc	actaaaactc	gcgaagctcg	gatcaaaaca	1131
132 gacattttct	ttgaaccgta	attaagctca	taaaaatatt	aattcatctt	gatggaatgc	1191
134 atatcataga	tgtactcaaa	catctcaaga	aagacctaa	attggatcaa	ctaatttagtt	1251
136 tgagaaaaaa	ttgctgtact	ttaagaata	tattaattta	aaaatttgct	gagtgaaatg	1311
138 atataatagt	cacaataatt	tttagttaaa	ctgctaaagc	attttgaata	gccgtgtac	1371
140 gcagatgcta	ctagacgcgg	tgtaaaagct	aatttttatt	taaaagctgt	cctaataattc	1431
142 cataaccatt	aatgtcccat	ttca gaa	ata agt tct	aat aaa gca	aaa ggt	1482
143			Glu Ile Ser	Ser Asn Lys	Ala Lys Gly	
144		155		160		

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146	caa	gca	gct	ggt	ggc	ggc	tgc	gaa	aca	ggt	tct	aca	tcc	agt	ttg	act	1530
147	Gln	Ala	Ala	Gly	Gly	Gly	Cys	Glu	Thr	Gly	Ser	Thr	Ser	Ser	Leu	Thr	
148			165					170							175		
150	gtc	aag	gaa	gaa	ccc	acc	gat	gtc	tta	ggc	agt	tta	gta	aat	atg	aaa	1578
151	Val	Lys	Glu	Glu	Pro	Thr	Asp	Val	Leu	Gly	Ser	Leu	Val	Asn	Met	Lys	
152			180					185							190		
154	aaa	gaa	gaa	aga	gaa	aat	cat	tcg	cca	acg	atg	tcc	cct	gtt	ggt	ttt	1626
155	Lys	Glu	Glu	Arg	Glu	Asn	His	Ser	Pro	Thr	Met	Ser	Pro	Val	Gly	Phe	
156			195					200							205		
158	ggt	tca	att	ggt	aat	gca	cag	gac	aac	tcc	gct	aca	ccg	ggtaagttt		1675	
159	Gly	Ser	Ile	Gly	Asn	Ala	Gln	Asp	Asn	Ser	Ala	Thr	Pro				
160	210				215				220								
162	aagagatcca	tataaagcaa	ataacaagaa	ttaatgtcag	ttaccaattt	tatttgatag											1735
164	tcaaagaact	actatagcga	tatctcctgc	cttttaattt	tatttttaatt	aggaaatacg											1795
166	aatatttcta	atttgtaaaa	taaaattgtat	taattaacta	gaattttaaaa	acctttgaa											1855
168	ttaggacata	cccttccaaa	aatcagtaat	cattggAAC	gagagtgtgg	tcccgaaagg											1915
170	gactactata	aaacctttt	agctatctga	tactgcacgc	tactaaaaat	gattagttt											1975
172	ggaaaatggg	tgtatTTT	taggaagtt	tcattttaga	agaaaatgtga	ttatTTTatt											2035
174	aaaccccttc	aagegaaact	acattttttc	tacgatattt	tggaaaaacaa	aatggtaag											2095
176	ttggaaagt	cctataaaac	agaattccac	ggtttcaa	actaaccagg	tttttgattt											2155
178	aattttgatt	aaatgagaaa	ttatcacact	tcagttaaaa	tgtttaattt	gattaagg	c										2215
180	ggacaatcac	agcagattt	catttttgcg	tgttatata	gaagtcgcct	tcacactt											2275
182	ctggcgcgc	tcaccactac	gtggagttcc	gccccgcagt	atttatata	atgattttac											2335
184	agttattttaa	tttttatgg	tgtatTTTaa	taaatatctt	atttatttcat	tttacata											2393
186	gtt	aaa	att	gaa	aga	att	tca	aac	gac	agt	acc	acg	gaa	aaa	aaa	gga	2441
187	Val	Lys	Ile	Glu	Arg	Ile	Ser	Asn	Asp	Ser	Thr	Thr	Glu	Lys	Lys	Gly	
188			225				230								235		
190	tcg	tcc	ttg	aca	atg	aat	aat	gac	gaa	atg	agc	atg	gaa	ggc	tgc	aat	2489
191	Ser	Ser	Leu	Thr	Met	Asn	Asn	Asp	Glu	Met	Ser	Met	Glu	Gly	Cys	Asn	
192			240				245								250		
194	cag	ttg	aat	ccc	gat	ttt	atc	aat	gaa	tct	tta	aat	aat	cct	gca	att	2537
195	Gln	Leu	Asn	Pro	Asp	Phe	Ile	Asn	Glu	Ser	Leu	Asn	Asn	Pro	Ala	Ile	
196	255						260									270	
198	tcg	agc	ata	tta	gta	agc	gga	gta	gga	cca	ata	ccc	gga	atc	gga	gtt	2585
199	Ser	Ser	Ile	Leu	Val	Ser	Gly	Val	Gly	Pro	Ile	Pro	Gly	Ile	Gly	Val	
200							275									285	
202	gga	gcg	ggg	acg	gga	aat	tta	ttg	act	gcc	aac	gcc	aat	gga	atc	tcc	2633
203	Gly	Ala	Gly	Thr	Gly	Asn	Leu	Leu	Thr	Ala	Asn	Ala	Asn	Gly	Ile	Ser	
204							290									300	
206	tcg	ggt	agc	agt	aat	tgt	ttg	gat	tac	atg	caa	cag	caa	aat	cac	ata	2681
207	Ser	Gly	Ser	Ser	Asn	Cys	Leu	Asp	Tyr	Met	Gln	Gln	Gln	Asn	His	Ile	
208							305								315		
210	tcc	gtg	ttt	tca	act	cag	ctg	gcc	aac	aaa	ggg	gcc	gaa	tca	gtt	tta	2729
211	Phe	Val	Phe	Ser	Thr	Gln	Leu	Ala	Asn	Lys	Gly	Ala	Glu	Ser	Val	Leu	
212							320								330		
214	agc	ggt	caa	ttt	caa	act	att	att	gcg	tat	cac	tgc	act	cag	cct	gct	2777
215	Ser	Gly	Gln	Phe	Gln	Thr	Ile	Ile	Ala	Tyr	His	Cys	Thr	Gln	Pro	Ala	
216	335						340									350	
218	aca	aaa	aqc	ttc	ctg	qaa	qac	ttt	ttt	atg	aaa	aac	cct	tta	aaq	att	2825

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223	Asn	Lys	Leu	Gln	Arg	His	Asn	Ser	Val	Gly	Met	Pro	Trp	Ile	Gly	Met		
224				370					375						380			
226	ggg	cag	gtt	gga	cta	act	cct	cct	aat	cct	gta	gcc	aaa	ata	aca	caa	2921	
227	Gly	Gln	Val	Gly	Leu	Thr	Pro	Pro	Asn	Pro	Val	Ala	Lys	Ile	Thr	Gln		
228				385					390						395			
230	cag	cag	cca	cat	aca	aag	acc	gta	ggc	cta	ttg	aaa	ccc	caa	ttc	aat	2969	
231	Gln	Gln	Pro	His	Thr	Lys	Thr	Val	Gly	Leu	Leu	Lys	Pro	Gln	Phe	Asn		
232				400					405						410			
234	caa	cat	gaa	aac	agc	aaa	cgt	agt	act	gta	agc	g	c	t	agc	aa	3017	
235	Gln	His	Glu	Asn	Ser	Lys	Arg	Ser	Thr	Val	Ser	Ala	Pro	Ser	Asn	Ser		
236	415				420					425						430		
238	ttt	gtc	gac	cag	tct	gat	cct	atg	ggc	aa	act	gaa	ttg	atg	tgc		3065	
239	Phe	Val	Asp	Gln	Ser	Asp	Pro	Met	Gly	Asn	Glu	Thr	Glu	Leu	Met	Cys		
240				435					440						445			
242	tgg	gaa	ggc	gga	tcc	tca	aa	cc	ag	tt	g	aa	tt	at	tg	c	3113	
243	Trp	Glu	Gly	Ser	Ser	Asn	Thr	Ser	Arg	Ser	Gly	Gln	Asn	Ser	Arg			
244				450					455						460			
246	aat	cat	gta	gac	agt	atc	agt	aca	tcc	agc	gag	tca	cag	gca	ata	aa	3161	
247	Asn	His	Val	Asp	Ser	Ile	Ser	Thr	Ser	Ser	Glu	Ser	Gln	Ala	Ile	Lys		
248				465					470						475			
250	ata	ctg	gaa	gca	gct	ggc	gtt	gat	ttg	gga	cag	gtc	aca	aaa	gga	ag	3209	
251	Ile	Leu	Glu	Ala	Ala	Gly	Val	Asp	Leu	Gly	Gln	Val	Thr	Lys	Gly	Ser		
252				480					485						490			
254	gat	cct	ggc	ctg	aca	act	gaa	aa	cc	att	gta	tca	ctg	caa	gg	gtt	3257	
255	Asp	Pro	Gly	Leu	Thr	Thr	Glu	Asn	Asn	Ile	Val	Ser	Leu	Gln	Gly	Val		
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258	aag	gtt	cca	gac	gaa	aa	cc	t	aca	cc	cag	cg	caa	cat	cg	gaa	3305	
259	Lys	Val	Pro	Asp	Glu	Asn	Leu	Thr	Pro	Gln	Gln	Arg	Gln	His	Arg	Glu		
260					515					520						525		
262	gaa	cag	ttg	gca	aaa	ata	aa	aa	atg	aat	caa	ttt	ctt	ttt	cct	gaa	3353	
263	Glu	Gln	Ile	Ala	Ile	Lys	Lys	Met	Asn	Gln	Phe	Leu	Phe	Pro	Glu			
264				530					535						540			
266	aat	gag	aat	tca	gta	gga	gct	aat	gta	agc	tca	cag	ata	aca	aa	att	3401	
267	Asn	Glu	Asn	Ser	Val	Gly	Ala	Asn	Val	Ser	Ser	Gln	Ile	Thr	Lys	Ile		
268					545					550						555		
270	cca	gga	gat	tta	atg	atg	ggg	atg	tcg	ggt	ggc	gga	ggc	g	tct	att	3449	
271	Pro	Gly	Asp	Leu	Met	Met	Gly	Met	Ser	Gly	Gly	Gly	Gly	Gly	Ser	Ile		
272				560					565						570			
274	ata	aat	ccg	ac	tg	cg	ca	ctg	cat	atg	cc	gg	aa	cc	aa	tc	3497	
275	Ile	Asn	Pro	Thr	Met	Arg	Gln	Leu	His	Met	Pro	Gly	Asn	Ala	Lys	Ser		
276	575					580					585					590		
278	gag	c	tc	t	tc	tc	q	ca	ag	tca	gga	ctt	tcg	gaa	gat	gta	at	3545
279	Glu	Leu	Leu	Ser	Ala	Thr	Ser	Ser	Gly	Leu	Ser	Glu	Asp	Val	Met	His		
280					595					600						605		
282	cca	ggg	gat	gtt	ata	tca	gat	atg	ggt	gcc	gta	ata	gga	tgt	aat	aat	3593	
283	Pro	Gly	Asp	Val	Ile	Ser	Asp	Met	Gly	Ala	Val	Ile	Gly	Cys	Asn	Asn		

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286	aat caa aaa acc agt gtg caa tgt gga tct gga gta ggt gtt gtc act			3641
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288	625	630	635	
290	gga aca act gca gct gga gta aat gtc aat atg cat tgc tca agc tcc			3689
291	Gly Thr Thr Ala Ala Gly Val Asn Val Asn Met His Cys Ser Ser Ser			
292	640	645	650	
294	ggc gcc ccg aat ggc aat atg atg gga agc tct acg gat atg cta gcc			3737
295	Gly Ala Pro Asn Gly Asn Met Met Gly Ser Ser Thr Asp Met Leu Ala			
296	655	660	665	670
298	tgc ttt ggc aac aca agc tgc aac gtc atc gga acg gcc cca gat atg			3785
299	Ser Phe Gly Asn Thr Ser Cys Asn Val Ile Gly Thr Ala Pro Asp Met			
300	675	680	685	
302	tct aag gaa gtt tta aat caa gat agc cga acc cat tca cat caa ggg			3833
303	Ser Lys Glu Val Leu Asn Gln Asp Ser Arg Thr His Ser His Gln Gly			
304	690	695	700	
306	gga gtt gct caa atg gag tgg tcg aag att caa cat caa ttt ttc gaa			3881
307	Gly Val Ala Gln Met Glu Trp Ser Lys Ile Gln His Gln Phe Phe Glu			
308	705	710	715	
310	gaa cgc ctc aag ggg ggc aag ccc aga caa gtc act gga act gta gta			3929
311	Glu Arg Leu Lys Gly Gly Lys Pro Arg Gln Val Thr Gly Thr Val Val			
312	720	725	730	
314	cca caa cag caa acc cct tct gga tct gtc aac tgc tta aac aac			3977
315	Pro Gln Gln Gln Thr Pro Ser Gly Ser Gly Asn Ser Leu Asn Asn			
316	735	740	745	750
318	cag gtg cga ccc ctg caa ggt cca cct cct tac cac tcc atc cag			4025
319	Gln Val Arg Pro Leu Gln Gly Pro Pro Pro Tyr His Ser Ile Gln			
320	755	760	765	
322	aga tct gcg tca gta cca ata gcc act caa tcg ccc aat ccc tcg agt			4073
323	Arg Ser Ala Ser Val Pro Ile Ala Thr Gln Ser Pro Asn Pro Ser Ser			
324	770	775	780	
326	cca aac aat cta tct ctc ccg tca ccg cgg aca acc gca gca gtc atg			4121
327	Pro Asn Asn Leu Ser Leu Pro Ser Pro Arg Thr Thr Ala Ala Val Met			
328	785	790	795	
330	gga ttg ccg acc aac tct cct agc atg gat gga aca gga tca tta tct			4169
331	Gly Leu Pro Thr Asn Ser Pro Ser Met Asp Gly Thr Gly Ser Leu Ser			
332	800	805	810	
334	gga tct gtt ccg caa gct aat act tcg acg gtt cag gca ggc aca aca			4217
335	Gly Ser Val Pro Gln Ala Asn Thr Ser Thr Val Gln Ala Gly Thr Thr			
336	815	820	825	830
338	aca gtg ctc tca gca aac aag aac tgt ttt cag gca gac acc cca tcg			4265
339	Thr Val Leu Ser Ala Asn Lys Asn Cys Phe Gln Ala Asp Thr Pro Ser			
340	835	840	845	
342	ccg tca aat caa aat cgt agt aga aat acc gga tcg tca agc gtt ctt			4313
343	Pro Ser Asn Gln Asn Arg Ser Arg Asn Thr Gly Ser Ser Val Leu			
344	850	855	860	
346	acg cat aac tta agc agc aac cca agt acc ccc tta tct cat cta tcc			4361
347	Thr His Asn Leu Ser Ser Asn Pro Ser Thr Pro Leu Ser His Leu Ser			
348	865	870	875	

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